Standardized and simple sub-fractionation of human plasma reveals enrichment of many low abundant hydrophobic proteins

Jessen, Flemming; Wulff, Tune

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Standardized and simple sub-fractionation of human plasma reveals enrichment of many low abundant hydrophobic proteins

Flemming Jessen and Tune Wulff
National Food Institute, DTU, Kgs. Lyngby, Denmark (fjes@food.dtu.dk)

Aim

Sub-fractionation of blood plasma

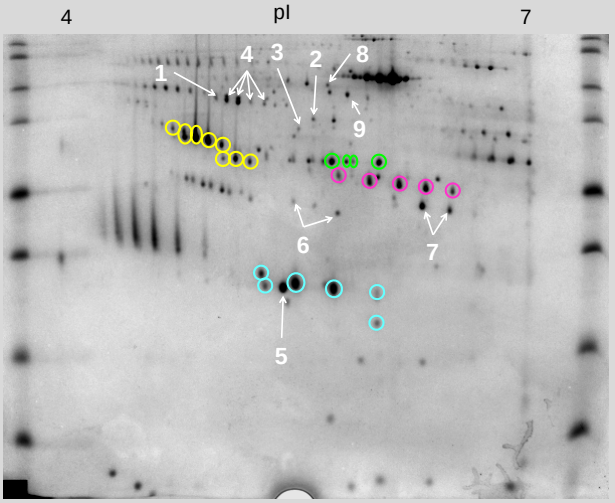
Analysis

Human plasma (2 µl) and proteins extracted from 400 µl plasma were analysed by 2DE (pI: 4-7 and 3-10; T: 12 %; Colloidal Coomassie staining)

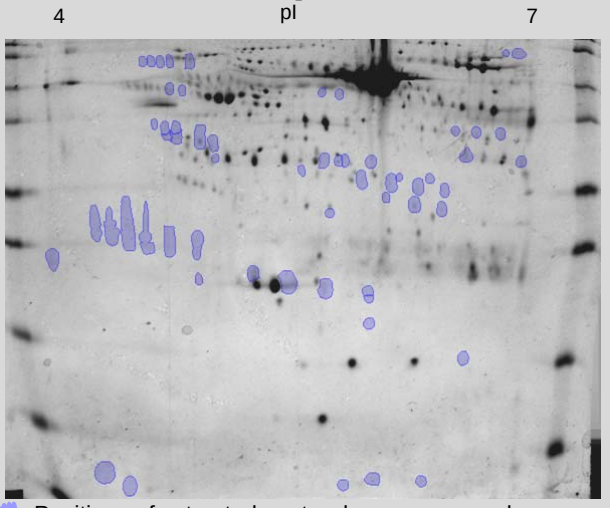
Background:

A main characteristic of plasma proteomics is the *10 order of magnitude problem,* causing that low abundance proteins are hard to visualise using 2D-gel electrophoresis (2DE). This problem calls for sub-fractionation to simplify the protein composition of the plasma sample, making it possible to detect lower abundant plasma proteins. Direction of strategies varies from depletion of high abundant proteins to enrichment of low abundant proteins using different approaches. However, a major concern when sub-fractionating is the reproducibility.

Extracted proteins

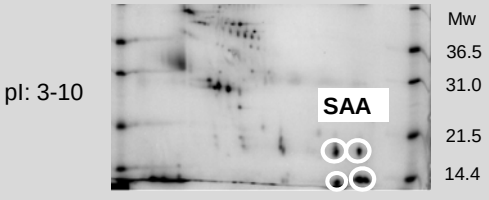


Blood plasma

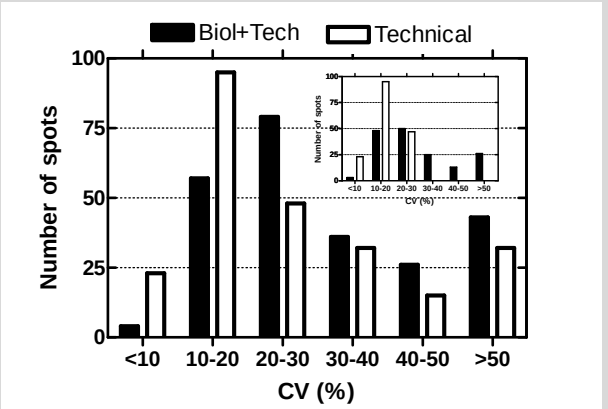


Positions of extracted spots where no or very low abundance spots are present in a 2D-gel of plasma

#	Protein ID (MALDI-TOF-TOF)
1	Actin, cytoplasmic 1
2	Actin, acrosomal process isoform
3	Adipocyte plasma membrane-associated protein
4	Alpha-1-antitrypsin
5	Apolipoprotein A-I
6	Apolipoprotein E
7	Ficolin-3
8	Lipopolysaccharide-binding protein
9	Prenylcysteine oxidase 1
○	Apolipoprotein M
○	Haptoglobin-related protein
○	Apolipoprotein L1
○	Serum paraoxonase/arylesterase 1
○	Serum amyloid A



Technical and biological variation



Data (normalised spot volumes) from 2DE analyses of 10 protein extracts made from 10 subjects (Biol+Tech) and 10 protein extracts made from a plasma pool (Technical)

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